

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/525, 178A  
Source: IFWO  
Date Processed by STIC: 09/14/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/525, 178A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII              The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please**  
                                  **ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length        Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                                  **each n or Xaa can only represent a single residue.** Please present the **maximum** number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)             . Normally, PatentIn would automatically generate this section from the  
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                  the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                                  **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)              (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)              <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)              Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                  scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                                  is Artificial Sequence. (see item 11 below)
  
- ~~11      Use of <220>        Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use  
                                  of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                                  Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as  
                                  explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of  
                                  Sequence Rules~~
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa        "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 09/14/2006

PATENT APPLICATION: US/10/525,178A

TIME: 10:29:25

Input Set : A:\14975WO.ST25.txt

Output Set: N:\CRF4\09142006\J525178A.raw

of

3 <110> APPLICANT: Hanski, Emanuel  
 4 Moses, Allon E  
 5 Hidalgo-Grass, Carlos  
 7 <120> TITLE OF INVENTION: Compositions and methods for the treatment and prophylaxis  
 8 infections caused by gram positive bacteria

10 <130> FILE REFERENCE: 73975/JPW/JW  
 12 <140> CURRENT APPLICATION NUMBER: US 10/525,178A  
 13 <141> CURRENT FILING DATE: 2005-02-22  
 15 <150> PRIOR APPLICATION NUMBER: IL 151436  
 16 <151> PRIOR FILING DATE: 2002-08-22  
 18 <150> PRIOR APPLICATION NUMBER: PCT/IL03/00687  
 19 <151> PRIOR FILING DATE: 2003-08-19  
 21 <160> NUMBER OF SEQ ID NOS: 32  
 23 <170> SOFTWARE: PatentIn version 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 19  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: m13/puc sequence primer (-20)  
 33 <400> SEQUENCE: 1  
 34 gtaaaaaaacg acggccagt 19  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 16  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Artificial Sequence  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: m13/puc reverse sequencing primer (-21) forward primer for  
 tag  
 44 amplification  
 46 <400> SEQUENCE: 2  
 47 aacagctatg accatg 16  
 50 <210> SEQ ID NO: 3  
 51 <211> LENGTH: 20  
 52 <212> TYPE: DNA  
 53 <213> ORGANISM: Artificial Sequence  
 55 <220> FEATURE:  
 56 <223> OTHER INFORMATION: Reverse primer for tag amplification  
 58 <400> SEQUENCE: 3  
 59 agcagttcgt agttatcttg 20  
 62 <210> SEQ ID NO: 4  
 63 <211> LENGTH: 19  
 64 <212> TYPE: DNA

Does Not Comply  
 Corrected Diskette Needed  
 (pg-5,6)

65 <213> ORGANISM: Artificial Sequence

• 7

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```

67 <220> FEATURE:
68 <223> OTHER INFORMATION: Inverse PCR primer from IRr
70 <400> SEQUENCE: 4
71 ttatcagcaa taaaccagc 19
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 18
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Inverse primer from IR1
82 <400> SEQUENCE: 5
83 aaagtcctcc tgggtatg 18
86 <210> SEQ ID NO: 6
87 <211> LENGTH: 20
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Inverse PCR primer from 3' of sile
94 <400> SEQUENCE: 6
95 tttggcagct ttgacgatgc 20
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 20
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Inverse PCR primer from 5' of Sila
106 <400> SEQUENCE: 7
107 tcttcaagca gctgattggg 20
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 23
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: 2598-2620 in sil
118 <400> SEQUENCE: 8
119 ggagttggtt tatcaaattgt cag 23
122 <210> SEQ ID NO: 9
123 <211> LENGTH: 23
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: 3213-3235 in sil
130 <400> SEQUENCE: 9
131 atctgccaca aagactgatac aag 23
134 <210> SEQ ID NO: 10
135 <211> LENGTH: 21
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:

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Input Set : A:\14975WO.ST25.txt

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```

140 <223> OTHER INFORMATION: 2013-2033 in sil
142 <400> SEQUENCE: 10
143 ttattggatc ggaacttacg c 21
146 <210> SEQ ID NO: 11
147 <211> LENGTH: 21
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: 3554-3574 in sil
154 <400> SEQUENCE: 11
155 tgcttcccaa caacttacca c 21
158 <210> SEQ ID NO: 12
159 <211> LENGTH: 22
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: 2088-2109 in sil
166 <400> SEQUENCE: 12
167 gctcgctata gtaagcaaat cg 22
170 <210> SEQ ID NO: 13
171 <211> LENGTH: 18
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: 5871-5888 in sil
178 <400> SEQUENCE: 13
179 cagcgattaa gcattgac 18
182 <210> SEQ ID NO: 14
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: 1616-1634 in sil
190 <400> SEQUENCE: 14
191 acgaaaggtc aatggttcac 20
194 <210> SEQ ID NO: 15
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: 2338-2357 in sil
202 <400> SEQUENCE: 15
203 aggtatggat aagcgttgag 20
206 <210> SEQ ID NO: 16
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: 3873-3894 in sil

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Input Set : A:\14975WO.ST25.txt

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214 <400> SEQUENCE: 16  
215 atgacacttg ttacacgtcc 20  
218 <210> SEQ ID NO: 17  
219 <211> LENGTH: 22  
220 <212> TYPE: DNA  
221 <213> ORGANISM: Artificial Sequence  
223 <220> FEATURE:  
224 <223> OTHER INFORMATION: 3873-3984  
226 <400> SEQUENCE: 17  
227 actagtcagc ttgacgaact tc  
230 <210> SEQ ID NO: 18  
231 <211> LENGTH: 19  
232 <212> TYPE: DNA  
233 <213> ORGANISM: Artificial Sequence  
235 <220> FEATURE:  
236 <223> OTHER INFORMATION: emm typing forward primer  
238 <400> SEQUENCE: 18  
239 tattcgctta gaaaattaa 19  
242 <210> SEQ ID NO: 19  
243 <211> LENGTH: 20  
244 <212> TYPE: DNA  
245 <213> ORGANISM: Artificial Sequence  
247 <220> FEATURE:  
248 <223> OTHER INFORMATION: emm typing reverse primer  
250 <400> SEQUENCE: 19  
251 gcaagttctt cagcttggtt 20  
254 <210> SEQ ID NO: 20  
255 <211> LENGTH: 28  
256 <212> TYPE: DNA  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: aad9 forward primer  
262 <400> SEQUENCE: 20  
263 ccatggtcct cgagctctag atcttaag 28  
266 <210> SEQ ID NO: 21  
267 <211> LENGTH: 25  
268 <212> TYPE: DNA  
269 <213> ORGANISM: Artificial Sequence  
271 <220> FEATURE:  
272 <223> OTHER INFORMATION: aad9 reverse primer  
274 <400> SEQUENCE: 21  
275 ctgcaggcgc ttaccaatta gaatg 25  
278 <210> SEQ ID NO: 22  
279 <211> LENGTH: 24  
280 <212> TYPE: DNA  
281 <213> ORGANISM: Artificial Sequence  
283 <220> FEATURE:  
284 <223> OTHER INFORMATION: 6873-6896 in JS95 sil, 5096-5119 in M1  
286 <400> SEQUENCE: 22

Insufficient Explanation.  
What is the source of genetic  
material? See <sup>22</sup>Item 11  
on Error Summary  
Sheet.

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Input Set : A:\14975WO.ST25.txt

Output Set: N:\CRF4\09142006\J525178A.raw

287 tcgatatgga gataaagaaa ctgg 24  
 290 <210> SEQ ID NO: 23  
 291 <211> LENGTH: 22  
 292 <212> TYPE: DNA  
 293 <213> ORGANISM: Artificial Sequence  
 295 <220> FEATURE:  
 296 <223> OTHER INFORMATION: 6804-6825 in M1 section 36  
 298 <400> SEQUENCE: 23  
 299 aacagtgcctt tcaggaactc ct 22  
 302 <210> SEQ ID NO: 24  
 303 <211> LENGTH: 22  
 304 <212> TYPE: DNA  
 305 <213> ORGANISM: Artificial Sequence  
 307 <220> FEATURE:  
 308 <223> OTHER INFORMATION: 10031-10052 in M1 section 36  
 310 <400> SEQUENCE: 24  
 311 ctaggtgcaa ttgaggagtc aa 22  
 314 <210> SEQ ID NO: 25  
 315 <211> LENGTH: 20  
 316 <212> TYPE: DNA  
 317 <213> ORGANISM: Artificial Sequence  
 319 <220> FEATURE:  
 320 <223> OTHER INFORMATION: 20-43 in JS95 sil, 7287-7306 section 152 in M1  
 322 <400> SEQUENCE: 25  
 323 tcctcgcaact gttccaatag 20  
 326 <210> SEQ ID NO: 26  
 327 <211> LENGTH: 20  
 328 <212> TYPE: DNA  
 329 <213> ORGANISM: Artificial Sequence  
 331 <220> FEATURE:  
 332 <223> OTHER INFORMATION: 3580-3599 in M1 section 36  
 334 <400> SEQUENCE: 26  
 335 aggtggtggtt ggagcaggta 20  
 338 <210> SEQ ID NO: 27  
 339 <211> LENGTH: 21  
 340 <212> TYPE: DNA  
 341 <213> ORGANISM: Artificial Sequence  
 343 <220> FEATURE:  
 344 <223> OTHER INFORMATION: 1545-1565 in M1 section 36  
 346 <400> SEQUENCE: 27  
 347 aagaagtgggt cccaatttct g 21  
 350 <210> SEQ ID NO: 28  
 351 <211> LENGTH: 30  
 352 <212> TYPE: DNA  
 353 <213> ORGANISM: Artificial Sequence  
 355 <220> FEATURE:  
 356 <223> OTHER INFORMATION: Forward all M primer with BamHI site  
 358 <400> SEQUENCE: 28  
 359 cctgaaaatg aggatccttc ctaaaaaacg 30

*Handwritten note: Same Error*



VERIFICATION SUMMARY

DATE: 09/14/2006

PATENT APPLICATION: US/10/525,178A

TIME: 10:29:26

Input Set : A:\14975WO.ST25.txt

Output Set: N:\CRF4\09142006\J525178A.raw